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**RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/219,442**

DATE: 03/08/1999  
TIME: 14:30:43

*INPUT SET: S30972.raw*

This Raw Listing contains the General Information Section and up to the first 5 pages.

**RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/219,442**DATE: 03/08/1999  
TIME: 14:30:44**INPUT SET: S30972.raw**

47                 (ix) TELECOMMUNICATION INFORMATION:  
48                         (A) TELEPHONE: (202)371-2600  
49                         (B) TELEFAX: (202)371-2540  
50  
51  
52         (2) INFORMATION FOR SEQ ID NO:1:  
53  
54                 (i) SEQUENCE CHARACTERISTICS:  
55                         (A) LENGTH: 1674 base pairs  
56                         (B) TYPE: nucleic acid  
57                         (C) STRANDEDNESS: double  
58                         (D) TOPOLOGY: linear  
59  
60                 (ii) MOLECULE TYPE: cDNA  
61  
62  
63                 (ix) FEATURE:  
64                         (A) NAME/KEY: sig\_peptide  
65                         (B) LOCATION: 12..80  
66  
67                 (ix) FEATURE:  
68                         (A) NAME/KEY: mat\_peptide  
69                         (B) LOCATION: 81..1268  
70  
71                 (ix) FEATURE:  
72                         (A) NAME/KEY: CDS  
73                         (B) LOCATION: 12..1268  
74  
75  
76  
77                 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
78  
79         GTCCTTCCAC C ATG CAC TCG CTG GGC TTC TTC TCT GTG GCG TGT TCT CTG         50  
80                 Met His Ser Leu Gly Phe Phe Ser Val Ala Cys Ser Leu  
81                 -23                 -20                 -15  
82  
83         CTC GCC GCT GCG CTG CTC CCG GGT CCT CGC GAG GCG CCC GCC GCC GCC         98  
84         Leu Ala Ala Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala  
85         -10                 -5                 1                 5  
86  
87         GCC GCC TTC GAG TCC GGA CTC GAC CTC TCG GAC GCG GAG CCC GAC GCG         146  
88         Ala Ala Phe Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala  
89                 10                 15                 20  
90  
91         GGC GAG GCC ACG GCT TAT GCA AGC AAA GAT CTG GAG GAG CAG TTA CGG         194  
92         Gly Glu Ala Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg  
93                 25                 30                 35  
94  
95         TCT GTG TCC AGT GTA GAT GAA CTC ATG ACT GTA CTC TAC CCA GAA TAT         242  
96         Ser Val Ser Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr  
97                 40                 45                 50  
98  
99         TGG AAA ATG TAC AAG TGT CAG CTA AGG AAA GGA GGC TGG CAA CAT AAC         290

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100	Trp Lys Met Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn			
101	55	60	65	70
102				
103	AGA GAA CAG GCC AAC CTC AAC TCA AGG ACA GAA GAG ACT ATA AAA TTT			338
104	Arg Glu Gln Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe			
105	75	80	85	
106				
107	GCT GCA GCA CAT TAT AAT ACA GAG ATC TTG AAA AGT ATT GAT AAT GAG			386
108	Ala Ala Ala His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu			
109	90	95	100	
110				
111	TGG AGA AAG ACT CAA TGC ATG CCA CGG GAG GTG TGT ATA GAT GTG GGG			434
112	Trp Arg Lys Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly			
113	105	110	115	
114				
115	AAG GAG TTT GGA GTC GCG ACA AAC ACC TTC TTT AAA CCT CCA TGT GTG			482
116	Lys Glu Phe Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val			
117	120	125	130	
118				
119	TCC GTC TAC AGA TGT GGG GGT TGC TGC AAT AGT GAG GGG CTG CAG TGC			530
120	Ser Val Tyr Arg Cys Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys			
121	135	140	145	150
122				
123	ATG AAC ACC AGC ACG AGC TAC CTC AGC AAG ACG TTA TTT GAA ATT ACA			578
124	Met Asn Thr Ser Thr Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr			
125	155	160	165	
126				
127	GTG CCT CTC TCT CAA GGC CCC AAA CCA GTA ACA ATC AGT TTT GCC AAT			626
128	Val Pro Leu Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn			
129	170	175	180	
130				
131	CAC ACT TCC TGC CGA TGC ATG TCT AAA CTG GAT GTT TAC AGA CAA GTT			674
132	His Thr Ser Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val			
133	185	190	195	
134				
135	CAT TCC ATT ATT AGA CGT TCC CTG CCA GCA ACA CTA CCA CAG TGT CAG			722
136	His Ser Ile Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln			
137	200	205	210	
138				
139	GCA GCG AAC AAG ACC TGC CCC ACC AAT TAC ATG TGG AAT AAT CAC ATC			770
140	Ala Ala Asn Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile			
141	215	220	225	230
142				
143	TGC AGA TGC CTG GCT CAG GAA GAT TTT ATG TTT TCC TCG GAT GCT GGA			818
144	Cys Arg Cys Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly			
145	235	240	245	
146				
147	GAT GAC TCA ACA GAT GGA TTC CAT GAC ATC TGT GGA CCA AAC AAG GAG			866
148	Asp Asp Ser Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu			
149	250	255	260	
150				
151	CTG GAT GAA GAG ACC TGT CAG TGT GTC TGC AGA GCG GGG CTT CGG CCT			914
152	Leu Asp Glu Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro			

**RAW SEQUENCE LISTING**  
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153	265	270	275	
154				
155	GCC AGC TGT GGA CCC CAC AAA GAA CTA GAC AGA AAC TCA TGC CAG TGT			962
156	Ala Ser Cys Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys			
157	280	285	290	
158				
159	GTC TGT AAA AAC AAA CTC TTC CCC AGC CAA TGT GGG GCC AAC CGA GAA			1010
160	Val Cys Lys Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu			
161	295	300	305	310
162				
163	TTT GAT GAA AAC ACA TGC CAG TGT GTA TGT AAA AGA ACC TGC CCC AGA			1058
164	Phe Asp Glu Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg			
165	315	320	325	
166				
167	AAT CAA CCC CTA AAT CCT GGA AAA TGT GCC TGT GAA TGT ACA GAA AGT			1106
168	Asn Gln Pro Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser			
169	330	335	340	
170				
171	CCA CAG AAA TGC TTG TTA AAA GGA AAG AAG TTC CAC CAC CAA ACA TGC			1154
172	Pro Gln Lys Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys			
173	345	350	355	
174				
175	AGC TGT TAC AGA CGG CCA TGT ACG AAC CGC CAG AAG GCT TGT GAG CCA			1202
176	Ser Cys Tyr Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro			
177	360	365	370	
178				
179	GGA TTT TCA TAT AGT GAA GAA GTG TGT CGT TGT GTC CCT TCA TAT TGG			1250
180	Gly Phe Ser Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp			
181	375	380	385	390
182				
183	CAA AGA CCA CAA ATG AGC TAAGATTGTA CTGTTTCCA GTTCATCGAT			1298
184	Gln Arg Pro Gln Met Ser			
185	395			
186				
187	TTTCTATTAT GGAAAACGT GTTGCCACAG TAGAACTGTC TGTGAACAGA GAGACCCTTG			1358
188				
189	TGGGTCCATG CTAACAAAGA CAAAAGTCTG TCTTTCTGA ACCATGTGGA TAACTTTACA			1418
190				
191	GAAATGGACT GGAGCTCATC TGCAAAAGGC CTCTTGTAAA GACTGGTTTT CTGCCAATGA			1478
192				
193	CCAAACAGCC AAGATTTCC TCTTGTGATT TCTTTAAAAG AATGACTATA TAATTTATTT			1538
194				
195	CCACTAAAAA TATTGTTCT GCATTCATTT TTATAGCAAC AACAAATTGGT AAAACTCACT			1598
196				
197	GTGATCAATA TTTTTATATC ATGCAAAATA TGTAAAAT AAAATGAAAA TTGTATTTAT			1658
198				
199	AAAAAAAAAAA AAAAAAA			1674
200				
201				
202	(2) INFORMATION FOR SEQ ID NO:2:			
203				
204	(i) SEQUENCE CHARACTERISTICS:			
205	(A) LENGTH: 419 amino acids			

**RAW SEQUENCE LISTING  
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206 (B) TYPE: amino acid  
207 (D) TOPOLOGY: linear  
208  
209 (ii) MOLECULE TYPE: protein  
210  
211 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
212  
213 Met His Ser Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala  
214 -23 -20 -15 -10  
215  
216 Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe  
217 -5 1 5  
218  
219 Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala  
220 10 15 20 25  
221  
222 Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser  
223 30 35 40  
224  
225 Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met  
226 45 50 55  
227  
228 Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln  
229 60 65 70  
230  
231 Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala  
232 75 80 85  
233  
234 His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys  
235 90 95 100 105  
236  
237 Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe  
238 110 115 120  
239  
240 Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr  
241 125 130 135  
242  
243 Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr  
244 140 145 150  
245  
246 Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu  
247 155 160 165  
248  
249 Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser  
250 170 175 180 185  
25

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**SEQUENCE VERIFICATION REPORT  
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